

FIG. 1

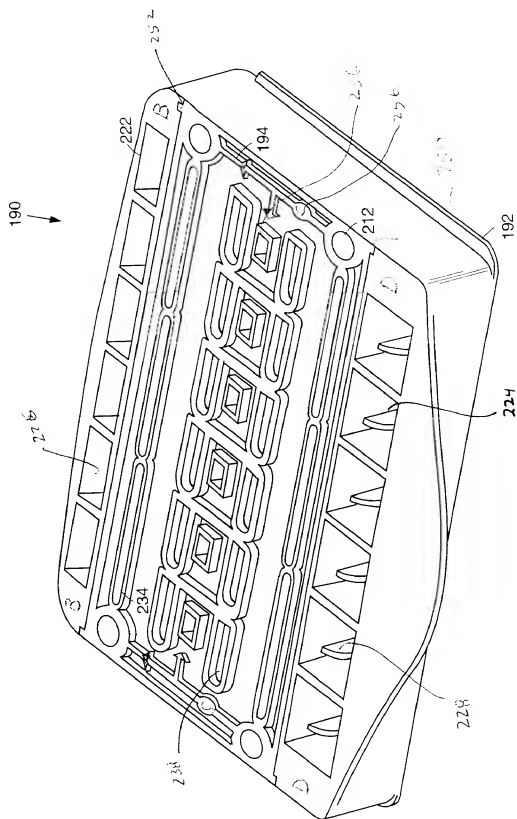


FIG. 2

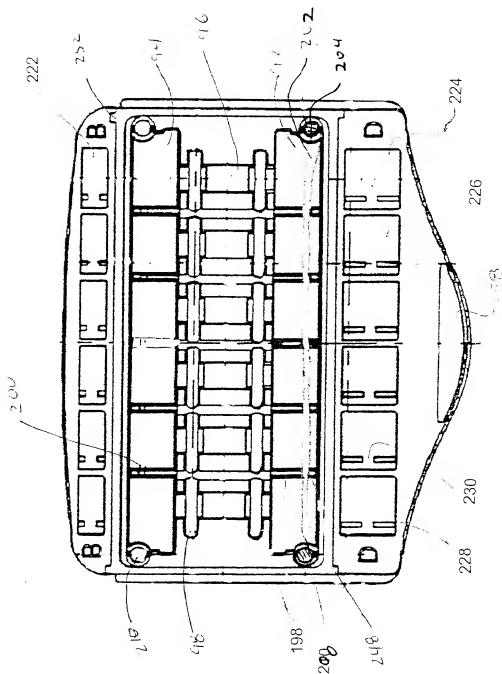
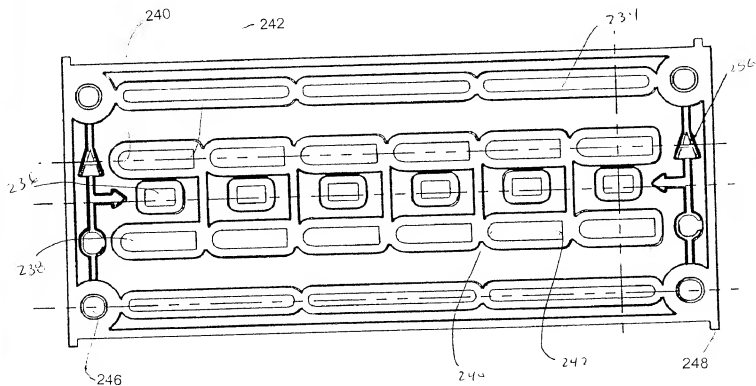
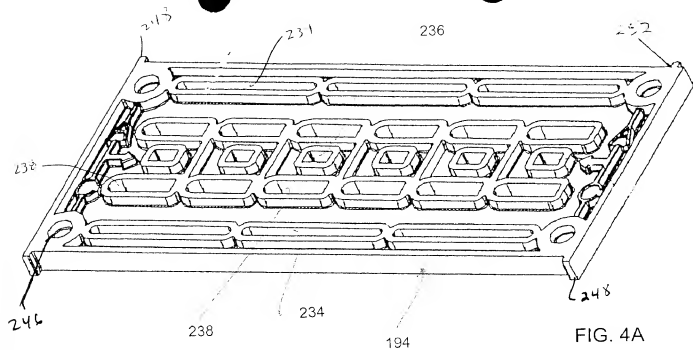


FIG. 3



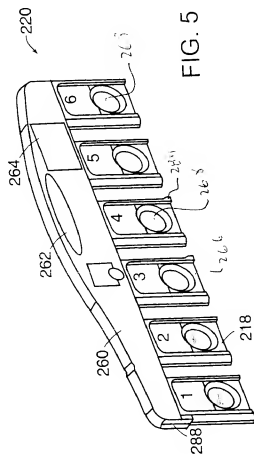


FIG. 5

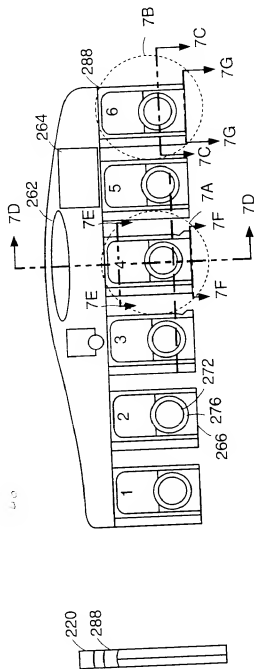


FIG. 6A



FIG. 6B



FIG. 7C

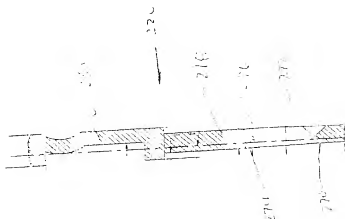


FIG. 7D

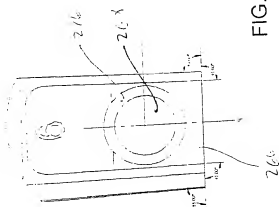
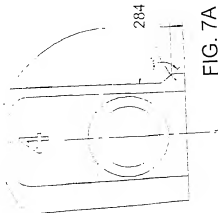
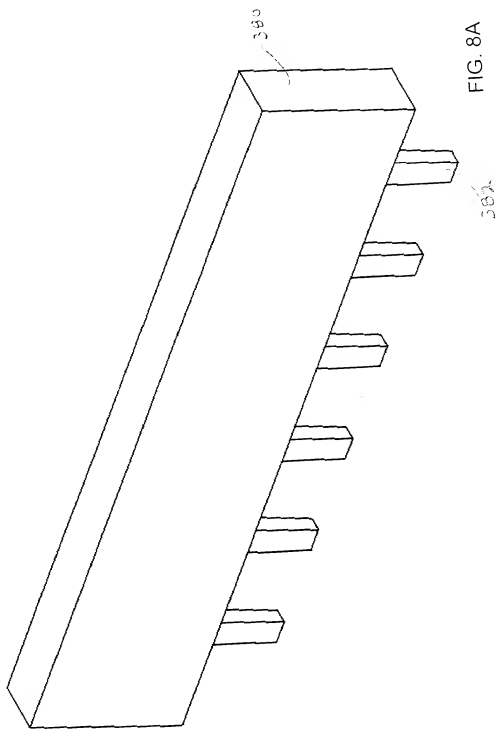


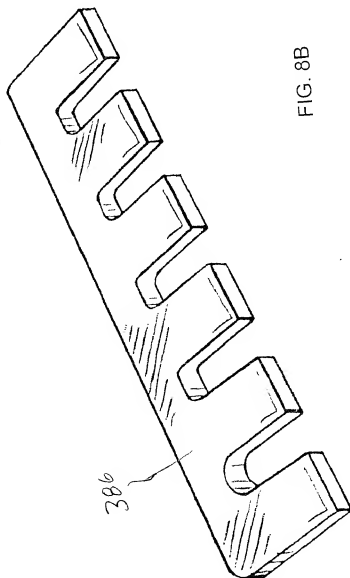
FIG. 7B



FIG. 7D







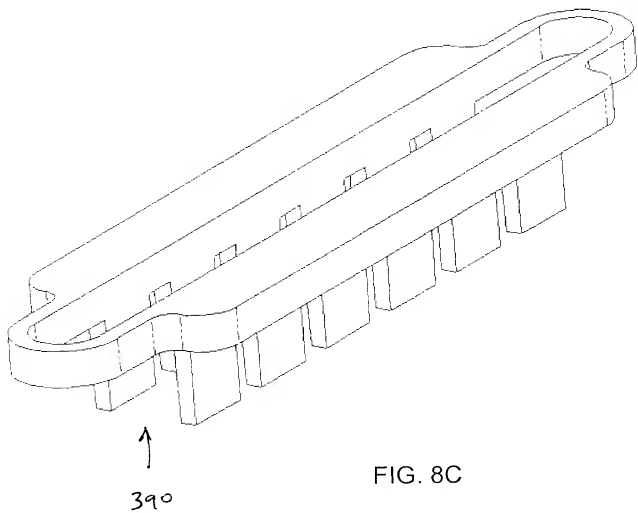


FIG. 8C

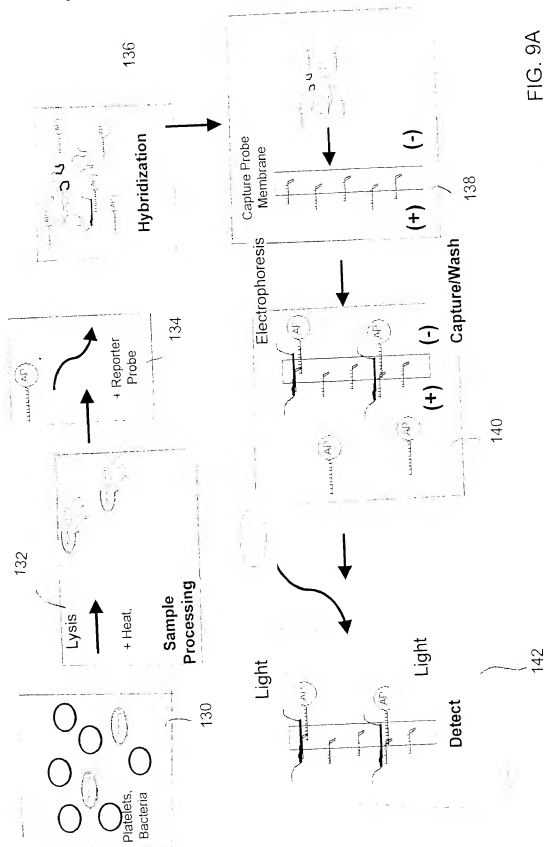


FIG. 9A

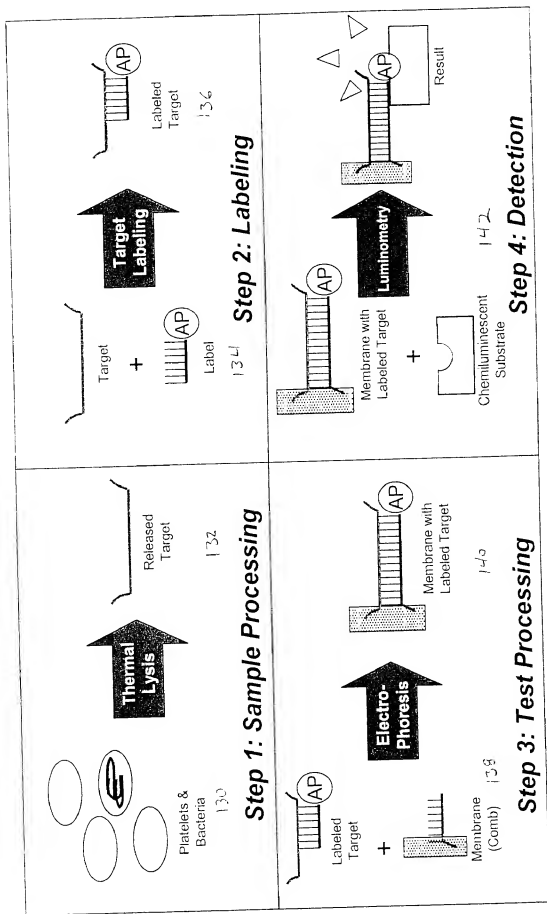


FIG. 9B

Staphylococcus species (* all unfinished)

staph_epi : CATGACATGTCAGGTCCTGACGGAAGCAGC : 198
 Staph_prob : -----CATGTCAGGTCCTGACGGAAGCAGC : 26
 saureus_co : CATGACATGTCAGGTCCTGACGGAAGCAGC : 200
 catgaaccATGTCAGGTCCTGACGGAAGCAGCattaaggatc tcata

Streptococcus species (* all unfinished)

Streppyog : CTGTCAGGTCCTGACGGAAGCAGC : 220
 Streppneum : GTTCAGGTCCTGACGGAAGCAGC : 92
 strep_targ : -----ATGTCAGGTCCTGACGGAAGCAGC : 26
 Strep_Equi : CTGTCAGGTCCTGACGGAAGCAGC : 135
 strepmutan : GGTTCAGGTCCTGACGGAAGCAGC : 221
 t tgcgtgaag GGTTCAGGTCCTGACGGAAGCAGC taagcg

Enterobacteriaceae, Pseudomonas aeruginosa, Bacillus cereus

* klebsyneum : GGTTCAGGTCCTGACGGAAGCAGC : 115
 * StaphilmurW : GGTTCAGGTCCTGACGGAAGCAGC : 84
 ecoli_comp : GGTTCAGGTCCTGACGGAAGCAGC : 84
 Ecoli_prob : GGTTCAGGTCCTGACGGAAGCAGC : 26
 pseuderaug : GGTTCAGGTCCTGACGGAAGCAGC : 84
 Bacillus_c : GGTTCAGGTCCTGACGGAAGCAGC : 194
 cgtcaacg cgt acc ggtTCAGGTCCTGACGGAAGCAGC a gc g gtgt

*unfinished sequence from genome centers FIG. 9C

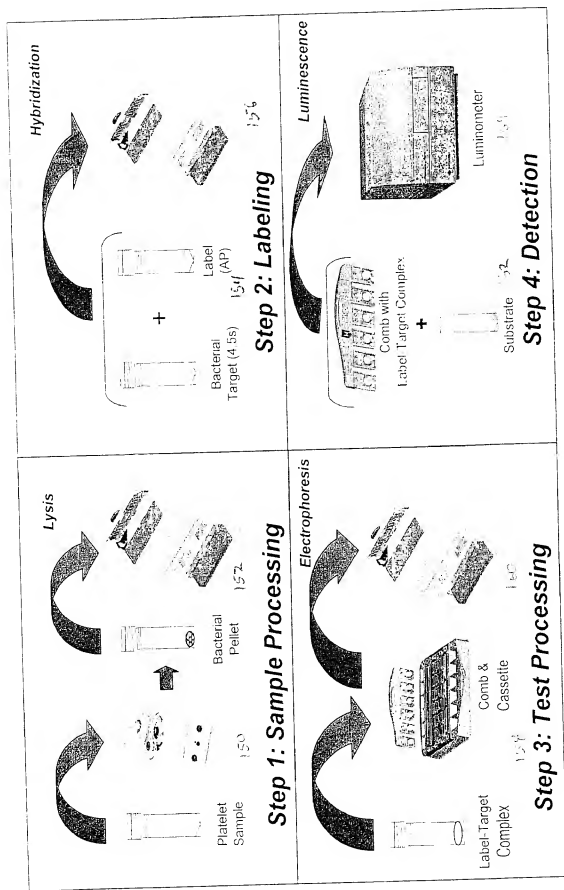
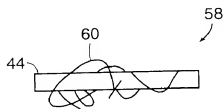
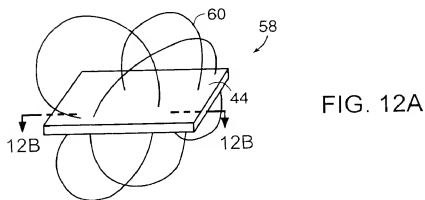
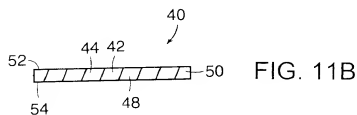
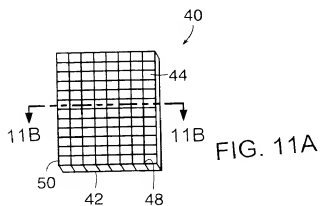


FIG. 10



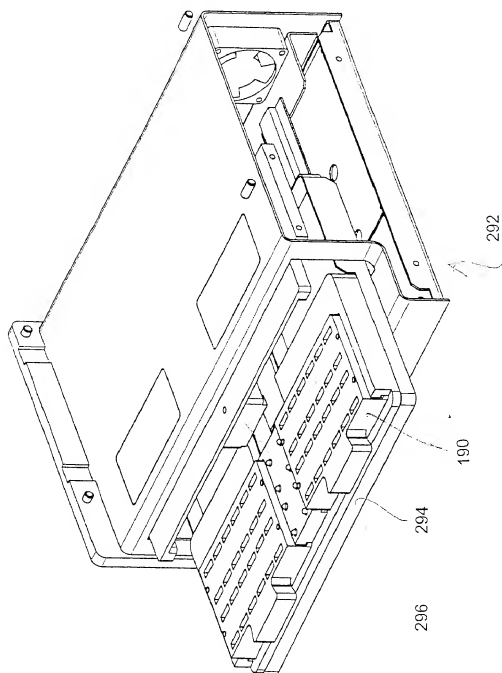


FIG. 13

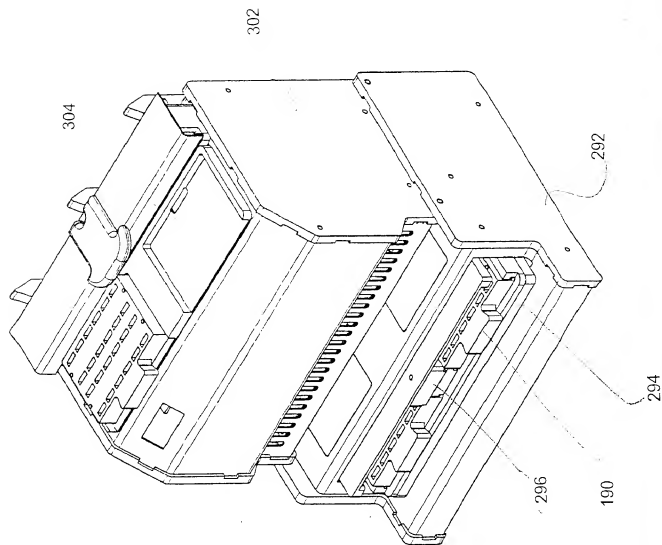
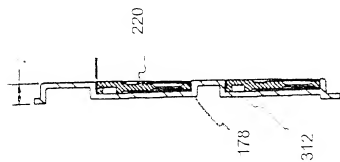
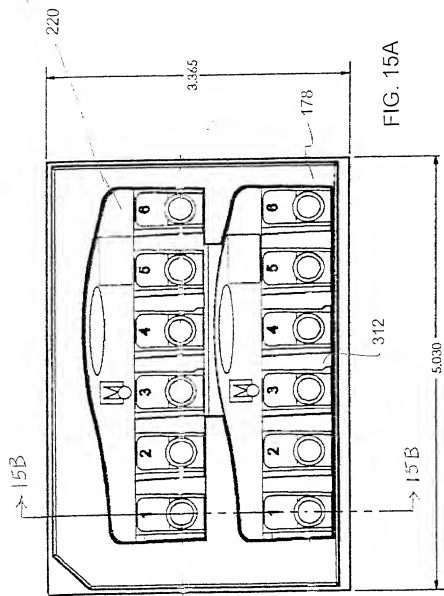


FIG. 14



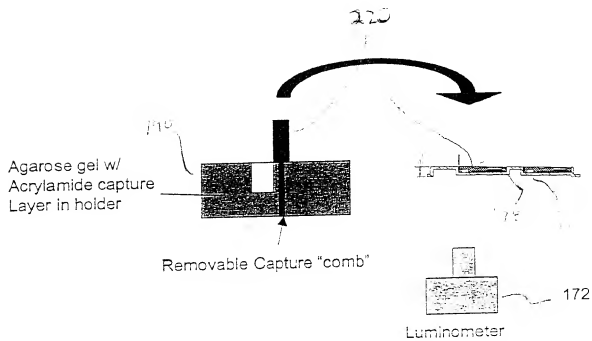


FIG. 16

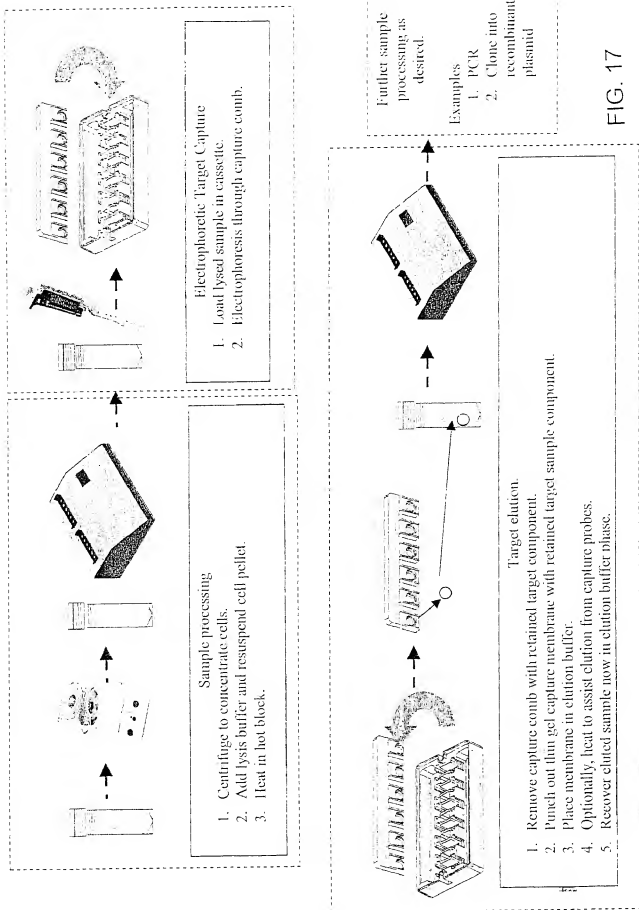


FIG. 17

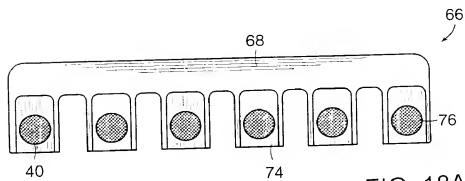


FIG. 18A

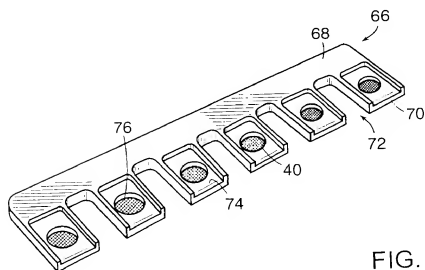
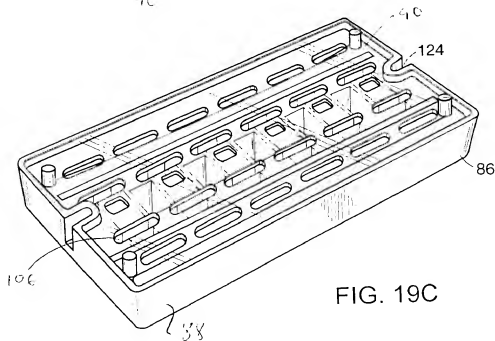
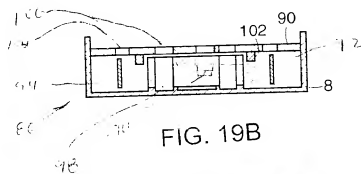
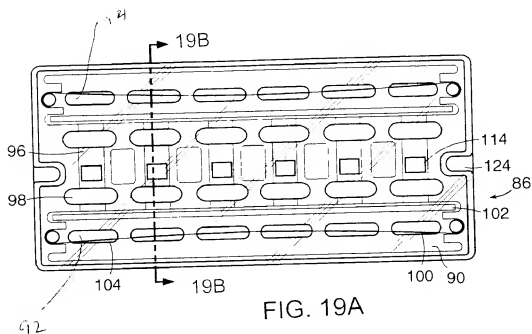


FIG. 18B



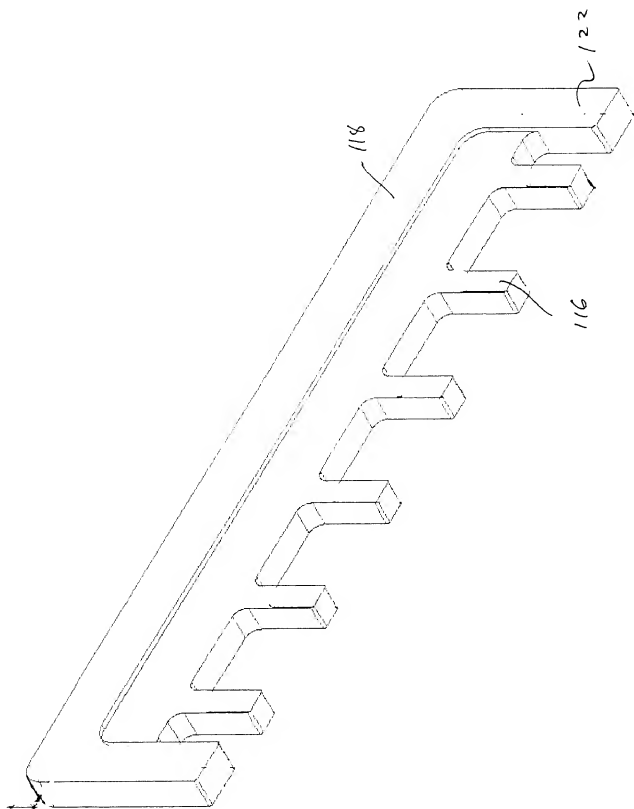


FIG. 20

FIG. 21A

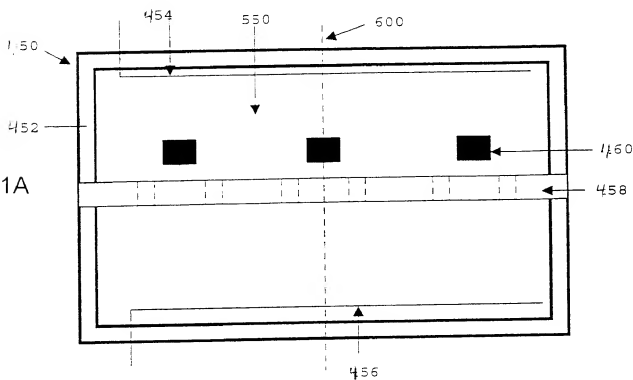


FIG. 21B

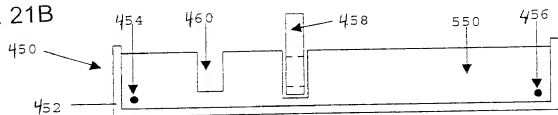
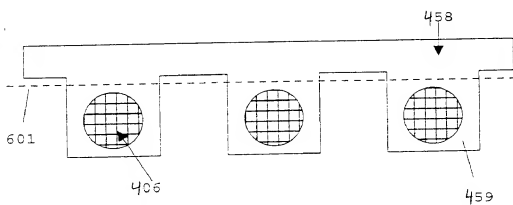


FIG. 21C



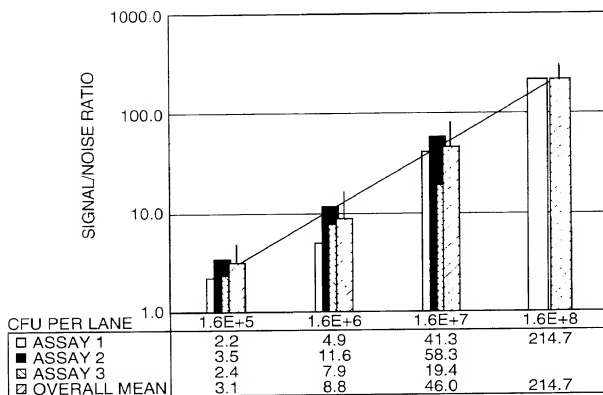
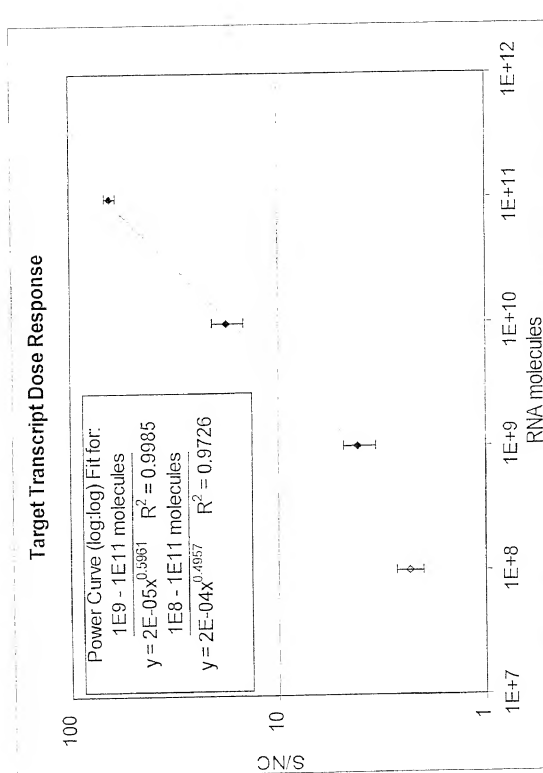
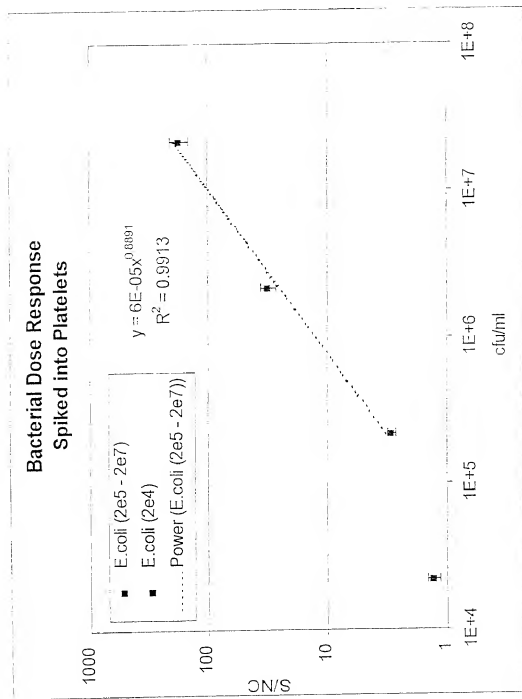


FIG. 22



- S/N from target transcripts spiked into assay after centrifugation step (mean \pm s.e. (n=13))
- Copy# of 4.5S in *E. coli* \sim 1,000/cfu

FIG. 23



- S/N from *E.coli* (n=8) spiked into negative platelets, then processed according to the assay scheme (mean \pm s.e.).

FIG. 24

Assay Time

Sample Processing

Target Enrichment 2min
 Rinse 2min
 Lysis 6min
 Cool 2min

12 - 15 minutes

45 - 50 minutes

Centrifuge samples x 1min
 Uncap, pour off liquid - BIOHAZARD
 Pipet Rinse Buffer
 Vortex to resuspend
 Centrifuge samples x 1min
 Uncap, pour off liquid - BIOHAZARD
 Pipet Lysis Buffer
 Vortex to resuspend
 Obtain NC and PC tubes
 Place NC, PC and sample tubes in heater
 Incubate through heat/cool cycle
 5min at >100C => 2min to 45C

Pipet Hybridization Buffer
 Mix by inversion several times
 Incubate 10min at 45C

Pipet 50ul from each tube into cassette
 Electrophorese for 20min

Assay

Probe Hybridization 11min
 Electrophoretic Capture 20min
 Wash 5min
 Detection 10min

Move comb to Wash Buffer 1
 Move comb to electroph wash slot
 Electrophorese for 3min
 Move comb to Conditioning Buffer
 Dry comb
 Pipet Substrate
 Load Reader
 Results Displayed

FIG. 25